

(FILE 'USPAT' ENTERED AT 12:11:21 ON 11 MAY 94)

L1 5233 S ?RELAXIN OR ?INSULIN OR ?INSULINLIKE OR IGF(W) (I OR II)
L2 433 S C(W) (CHAIN OR PEPTIDE)
L3 1265540 S MODIFI? OR ALTER? OR SHORTEN? OR TRUNCAT?
L4 126 S L1 AND L2
L5 110 S L3 AND L4
L6 45 S L2(P)L3

1. 5,304,473, Apr. 19, 1994, A-C-B proinsulin, method of manufacturing and using same, and intermediates in insulin production; Rama M. Belagaje, et al., 435/69.7, 252.33; 514/3; 530/303, 350; 536/23.51 [IMAGE AVAILABLE]

27. 4,639,333, Jan. 27, 1987, Process for converting preproinsulin analogs into insulins; Rainer Obermeier, et al., 530/303, 305; 930/10, 260 [IMAGE AVAILABLE]

01/10/94

> O <
OI IO IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : A-GeneSeq 13, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 1 Median 3 Standard Deviation 1.31
Times: CPU 00:00:24.10 Total Elapsed 00:01:29.00

Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4795

Sequence Name	Description	Length	Score	Init. Opt.
1. R23998	EGF/HB-EHM.	208	8	8
2. P81758	Sequence encoded by env gene	735	8	8
3. R24126	SIVmac239 env gene product.	879	8	8
4. P80805	Sequence of env protein of SI	880	8	8
**** 4 standard deviations above mean ****				
1. US-08-080-354B-3 (1-13)				

R23998 EGF/HB-EHM.

ID R23998 standard; Protein; 208 AA.
AC R23998;

DT 09-NOV-1992 (first entry)

DE EGF/HB-EHM.

KW Heparin-binding epidermal growth factor; EGF; HB-EHM;

X 10 X
KRKPTGYGSRKKR

III I I III
90 X 100 X 110

LATPNKEHGKRRKKKGKGLGKRRDPCLRKYKDF

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 1.07
Times: CPU 00:01:09.13 Total Elapsed 00:04:16.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4792

Sequence Name	Description	Length	Score	Init. Opt.
1. WMVETC	8K protein - turnip crinkle v	72	8	8
2. A37300	heparin-binding EGF-like grow	86	8	8
3. A38432	heparin-binding EGF-like grow	208	8	8
4. A41914	diphtheria toxin receptor prec	208	8	8
5. VCLJ52	env polyprotein precursor - s	880	8	8
6. S03068	env protein - Human T-cell ly	881	8	8
7. VCLJG3	env polyprotein - simian immu	881	8	8
8. VCLJG5	env polyprotein - simian immu	889	8	8
**** 5 standard deviations above mean ****				
1. US-08-080-354B-3 (1-13)				

WMVETC 8K protein - turnip crinkle virus

X 10 X
KRKPTGYGSRKKR

III I I III
20 30 40

NSLSDSDATGKRRKKGGEKSAKRRKLVASHAASSV

Results of the initial comparison of US-08-080-354B-3 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2

Mismatch penalty
Gap penalty

Cutoff score

Optimized scores

Scores:	Mean	Median	Standard Deviation
	2	3	0.94
Times:	CPU	Total Elapsed	
	00:00:48.06	00:02:50.00	
Number of residues:	11484420		
Number of sequences searched:	33329		
Number of scores above cutoff:	4191		
Sequence Name	Description	Length	Init. Opt. Score
1. VP8_TCV	**** 6 standard deviations above mean ***	72	8
2. ENV_S1VM2	P8 PROTEIN. POLYPROTEIN GP160 PR	380	8
3. ENV_S1VM1	ENVELOPE POLYPROTEIN GP160 PR	880	8
4. ENV_S1VMK	ENVELOPE POLYPROTEIN GP160 PR	881	8
5. ENV_S1VM1	ENVELOPE POLYPROTEIN GP160 PR	882	8
			6.36 0
			6.36 0
			6.36 0
			6.36 0
			6.36 0
			6.36 0
1. US-08-080-354B-3 (1-13)			
VP8_TCV	P8 PROTEIN.		
OS	TURNIP CRINKLE VIRUS (TCV).		
OC	VIRIDAE; SS-RNA NONENVELOPED VIRUSES; CARMOVIRIDAE.		
	X 10 X		
	KRKPTGYGSRKKR		
	NSLSDSDATGKRKKGGEKSAKRLVASHAASSV		
10	20 30 40		
Results of the initial comparison of US-08-080-354B-6 (1-13) with: Data bank : A-Geneseq 13, all entries			
PARAMETERS			
Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	13

Cutoff score

Initial scores to

1

*
DE Amino acid sequence of open reading frame upstream of lysin gene on
DE fragment of lambda.gt10-lysin4

KW Bacteriophage phi-vML3; lambda .gt 10-lysin4.

X 10 X

DKKRTGYGSRRRK

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EFPSKKDEGTGYAFRKGQLYVGSIK

X 10 X 20

Results of the initial comparison of US-08-080-354B-6 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1.00	Joining penalty	20
Gap penalty	0.05	Window size	13
Cutoff score	0		
Randomization group	0		

Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	2	3	1.07

Times: CPU 00:01:18.05 Total Elapsed 00:04:40.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4868

Sequence Name	Description	Length	Score	Init. Opt.	Sig.	Frame
**** 4 standard deviations above mean ****						
1. S08555	ribosomal protein L15 - Halob	29	7	7	4.69	0
2. S07769	histone H2B.3, sperm - sea ur	51	7	7	4.69	0
3. B32476	hypothetical protein - mouse	111	7	7	4.69	0
4. HSUR6P	histone H2B.2, sperm - sea ur	143	7	7	4.69	0
5. HSURB2	histone H2B.2, sperm - sea ur	143	7	7	4.69	0
6. HSURB1	histone H2B.2, sperm - sea ur	144	7	7	4.69	0
7. HSUR8P	histone H2B.3, sperm - sea ur	148	7	7	4.69	0
8. R5MXE	ribosomal protein L19.eR - Me	149	7	7	4.69	0
9. D22735	hypothetical nox3 protein - E	334	7	7	4.69	0
10. S12190	mobL protein - Thiobacillus f	378	7	7	4.69	0
11. A44056	nucleocapsid protein - canine	382	7	7	4.69	0
12. S07824	hypothetical protein 1 - fruit	633	7	7	4.69	0
13. S14382	hypothetical protein - fruit	984	7	7	4.69	0
**** 3 standard deviations above mean ****						
14. S02786	protamine 2a - horse (fragmen	25	6	6	3.75	0
15. A34356	protamine - Japanese quail	57	6	6	3.75	0
16. S10754	Protamine St2a - Horse	62	6	6	3.75	0
17. A34326	Protamine - chicken	62	6	7	3.75	0
18. S18671	Heat shock protein 70 (Ssp1)	65	6	6	3.75	0

19. GACH	galline - chicken	65	6	7	3.75	0
20. A03316	homeotic protein AC1 - Africa	67	6	6	3.75	0
21. JN0416	PabH protein - Rye	73	6	6	3.75	0
22. S01386	photosystem II phosphoprotein	73	6	6	3.75	0
23. S04148	photosystem II phosphoprotein	73	6	6	3.75	0
24. F2WTH	photosystem II phosphoprotein	73	6	6	3.75	0
25. F2ZMBH	photosystem II phosphoprotein	73	6	6	3.75	0
26. S04144	ribosomal protein S19 - Yersia	74	6	6	3.75	0
27. B41034	cytochrome-c oxidase chain VI	83	6	6	3.75	0
28. S06037	hypothetical protein - Serrat	84	6	6	3.75	0
29. S31482	sperm-specific protein Phi-1	92	6	6	3.75	0
30. R3EC19	ribosomal protein S19 - Esche	92	6	6	3.75	0
31. S08639	Homeotic protein zf-61 - Zebr	96	6	6	3.75	0
32. JC1195	plasmidogen-related protein B	96	6	6	3.75	0
33. S03334	hypothetical protein 1 - Lact	97	6	6	3.75	0
34. S22454	REP protein - Wood tobacco (f	101	6	6	3.75	0
35. A43262	orf 2-hit - Bdellovibrio bact	101	6	6	3.75	0
36. PW0018	hypothetical protein 105 - Mi	105	6	6	3.75	0
37. PW0017	hypothetical protein 105 (grm	105	6	6	3.75	0
38. S19375	dihydroflavonol 4-reductase -	109	6	6	3.75	0
39. S34648	proteinase inhibitor precurs	114	6	6	3.75	0
40. S04158	adrenergic receptor beta-2 -	125	6	6	3.75	0
41. S31617	Protamine - Boll weevil	132	6	6	3.75	0
42. S10305	fau protein - Mouse	133	6	6	3.75	0
43. S21452	ubiquitin-like protein / ribo	133	6	6	3.75	0
44. S18101	ubiquitin-like protein / ribo	133	6	6	3.75	0
45. JC1278		133	6	6	3.75	0

1. US-08-080-354B-6 (1-13)

S08555 ribosomal protein L15 - Halobacterium cutirubrum

Initial Score	=	7	Optimized Score	=	7	Significance	=	4.69
Residue Identity	=	53%	Matches	=	7	Mismatches	=	6
Gaps	=	0	Conservative Substitutions	=			=	0

X 10 X

DKKRTGYGSRRRK

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TDKRRRGSRTHGGGTHKNSRGA

X 10 X 20

Results of the initial comparison of US-08-080-354B-6 (1-13) with:
Data bank : Swiss-Prot 27, all entries

Similarity matrix	Unitary	K-tuple	2
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	13
Gap size penalty	0.05		
Cutoff score	0		
Randomization group	0		
Initial scores to save	45	Alignments to save	15
Optimized scores to save	0	Display context	10
SEARCH STATISTICS			

Scores: Mean 2 Median 3 Standard Deviation 0.94
Times: CPU 00:00:44.07 Total Elapsed 00:02:39.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4275

Sequence Name	Description	Length	Score	Opt.
1. RL16 HALCU	50S RIBOSOMAL PROTEIN HL16 (F	29	7	7
2. H2B3 ECHES	HISTONE H2B.3, SPERM (FRAGMENT)	40	7	7
3. H2B2 LVTPI	HISTONE H2B.2, SPERM.	142	7	7
4. H2B2 STRPU	HISTONE H2B.2, SPERM.	143	7	7
5. H2B2 PARAN	HISTONE H2B.2, SPERM.	143	7	7
6. H2B3 METVA	PROBABLE 50S RIBOSOMAL PROTEIN	148	7	7
7. MOBL_THIFE	MOBILIZATION PROTEIN MOBL.	378	7	7
8. ZFPA EPIVI	ZFPA PROTEIN (DEDB PROTEIN) (493	7	7
9. NOF1 DROME	71 KD PROTEIN IN NOF-FB TRANS	633	7	7
10. NOF1 DROME	112 KD PROTEIN IN NOF-FB TRANS	984	7	7
11. SWH1_YEAST	SWH1 PROTEIN.	1141	7	7

1. US-08-080-354B-6 (1-13)
RL16 HALCU 50S RIBOSOMAL PROTEIN HL16 (FRAGMENT). DE 50S RIBOSOMAL
PROTEIN HL16 (FRAGMENT).
OS HALOBACTERIUM CUTIRUBRUM.
X 10 X

DKKRTGYGSRRRK
|||||

TDKRRQRGSRTHGGGTHKNRGA
X 10 X 20

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : A-GeneSeq 13, all entries
PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05

Cutoff score 0

Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 1 Median 3 Standard Deviation 1.31

Times: CPU 00:00:23.03 Total Elapsed 00:01:31.00

Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4673

Sequence Name	Description	Length	Score	Opt.
1. R22590	Nonlinear peptide 8deltaTNF(1	22	7	7
2. R13070	SIV500 fusion protein.	12	6	6
3. R03460	Intracellular retention motif	48	6	6
4. R04933	Interferon-gamma receptor seg	223	6	6
5. P60518	Sequence of bovine inhibin B	288	6	6
6. R34544	Tet e gene product from pMW10	314	6	7
7. R37873	Tet e gene product from pMW10	314	6	7
8. R29623	Tet e gene product from pMW10	314	6	7
9. R20991	Protein "d" encoded by mycobact	314	6	7
10. R25853	MSH-dependent protein obtd. f	354	6	7
11. R32108	Pectin esterase	389	6	6
12. P80300	Pectin esterase.	389	6	6
13. R32020	Sequence of a eukaryotic tran	414	6	6
14. R28956	HIV gp160-MN precursor up to	513	6	7
15. P61363	Soybean glycinin A5A4B3 subun	561	6	6
16. R34938	Human glucose regulated prote	656	6	7
17. P81758	Sequence encoded by env gene	735	6	7
18. R13786	HIV multifunctional fusion po	770	6	6
19. R14903	HIV-1(MN) env protein.	856	6	7
20. R14904	HIV-1(MN-ST1) env protein.	857	6	7
21. R24126	SIVmac239 env gene product.	879	6	8
22. P80805	Sequence of env protein of SI	880	6	7
23. R10333	Deduced sequence of tomato ni	911	6	6
24. R20027	C-terminal amidation enzyme.	953	6	6
25. R11113	Equine C-terminal amidating e	980	6	6
26. R20025	C-terminal amidation enzyme.	1020	6	6
27. R35547	Sequence of the alpha 1C huma	1967	6	6
28. R35081	ZYMV polyprotein.	3080	6	6
29. P81769	Sequence encoded by top readi	3211	6	6
30. R37619	Sequence of the C-chain/A-cha	7	5	5
31. R29298	Nerve growth stimulating prot	9	5	5
32. R36857	Insulin-like growth factor-I	10	5	5
33. R37513	30Arg, 32Tyr 22-32 Peptide C	11	5	5
34. R36911	Insulin-like growth factor-II	12	5	5
35. R12491	Lys(342)-alpa-1-antitrypsin d	12	5	5
36. P80993	Sequence of unique protease y	13	5	5
37. R36856	Insulin-like growth factor-I	14	5	6
38. R26100	Proposed Superantigen binding	15	5	6
39. R10929	Relaxin C peptide epitope II.	15	5	6
40. R36852	Insulin-like growth factor-I	18	5	7
41. R36848	Insulin-like growth factor-I	18	5	7
42. R28791	High endotoxin affinity polyp	18	5	5
43. R28790	High endotoxin affinity polyp	18	5	5
44. R28787	High endotoxin affinity polyp	18	5	5
45. R28783	High endotoxin affinity polyp	18	5	5

1. US-08-080-354B-7 (1-13)

R22590 Nonlinear peptide 8deltaTNF(144-157). KW Tumour necrosis
factor; TNFalpha; polylysine.
OS Synthetic.

X 10 X

DKKRTGYGSRKKR

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DYLAGFKAHGKRYGGGRKKG

10 20 X

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : PIR 38, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 2 3 1.09
Times: CPU Total Elapsed
 00:01:14.01 00:03:57.00

Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4955

Sequence Name	Description	Length	Score	Opt.	Frame
1. D22735	*** 6 standard deviations above mean ***				
2. JCI1409	hypothetical nox3 protein - E 334	9	6.42	0	
	*** 5 standard deviations above mean ***				
	heparin-binding EGF-like grow 208	8	5.50	0	
	*** 4 standard deviations above mean ***				
3. S08555	ribosomal protein L15 - Halob	29	7	4.58	0
4. S16512	Hypothetical protein - Yeast	182	7	4.58	0
5. JCI1410	heparin-binding EGF-like grow	208	7	4.58	0
6. S33114	DIOR COP protein - variola vi	248	7	4.58	0
7. G36847	FIOR protein - variola virus	248	7	4.58	0
	DNA-(apurinic or apyrimidin	367	7	4.58	0
	secY protein - Mycoplasma cap	482	7	4.58	0
	cytochrome d complex terminal	523	7	4.58	0
11. B43827	heat shock protein groEL - Br	544	7	4.58	0
12. A36705	transcriptional activator fhl	686	7	4.58	0
13. S12079	fhlA protein - Escherichia co	692	7	4.58	0
14. A25064	regulatory protein ARGRII - y	880	7	4.58	0
15. A41667	nitrate reductase (NADH) - wi	918	7	4.58	0
16. VCLJCC	env polyprotein precursor - c	966	7	4.58	0

1. US-08-080-354B-7 (1-13)

D22735 hypothetical nox3 protein - Emericella nidulans
Initial Score = 9 Optimized Score = 6.42
Residue Identity = 69% Matches = 9 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

X 10 X
DKKRTGYGSRKKR

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HSLDVSLAYIYIKRGLGVSVKVKKNNAFLIIV

110 X 120 X 130

Results of the initial comparison of US-08-080-354B-7 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean Median Standard Deviation
 2 3 0.97
Times: CPU Total Elapsed
 00:00:44.00 00:02:35.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4341

Sequence Name	Description	Length	Score	Opt.	Frame
1. RL16 HALCU	*** 5 standard deviations above mean ***				
2. RL34 BORBU	50S RIBOSOMAL PROTEIN HL16 (F	29	7	5.14	0
3. TPM_HANPO	50S RIBOSOMAL PROTEIN L34.	51	7	5.14	0
4. VD10 VARV	TROPOMYOSIN-LIKE PROTEIN (FRA	182	7	5.14	0
5. APN1 YEAST	PROTEIN D10.	248	7	5.14	0
6. SECY_MYCCA	DNA-(APURINIC OR APYRIMIDINIC	361	7	5.14	0
7. CYDA_ECOLI	PREPROTEIN TRANSLOCASE SECY S	482	7	5.14	0
8. FHIA_ECOLI	CYTOCHROME D UBIQUINOL OXIDAS	522	7	5.14	0
9. ENV_HV128	FORMATE HYDROGENLYASE TRANSCR	692	7	5.14	0
10. ARG2 YEAST	ENVELOPE POLYPROTEIN GP160 PR	863	7	5.14	0
11. NIA_CUWA	ARGININE METABOLISM REGULATIO	880	7	5.14	0
12. ENV_CAEVC	NITRATE REDUCTASE (EC 1.6.6.1	918	7	5.14	0
	ENV POLYPROTEIN PRECURSOR (CO	966	7	5.14	0

1. US-08-080-354B-7 (1-13)

RL16 HALCU 50S RIBOSOMAL PROTEIN HL16 (FRAGMENT). DE 50S RIBOSOMAL
PROTEIN HL16 (FRAGMENT).
OS HALOBACTERIUM CUTIRUBRUM.
X 10 X

DKKRTGYGSRKKR

||||| |||||

TDKRRQRGSRTHGGGTHKNSRGA

X 10 X 20

Results of the initial comparison of US-08-080-354B-8 (1-13) with:
Data bank : A-Geneseq 13, all entries

PARAMETERS

Similarity matrix K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0
Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10
SEARCH STATISTICS
Scores: Mean 1 Median 3 Standard Deviation 1.32
Times: CPU 00:00:24.10 Total Elapsed 00:01:35.00
Number of residues: 4624329
Number of sequences searched: 37412
Number of scores above cutoff: 4840
Sequence Name Description Length Score Init. Opt.
1. R36857 Insulin-like growth factor-I 10 7 8 4.55 0
2. R36911 Insulin-like growth factor-II 12 7 8 4.55 0
3. R36852 Insulin-like growth factor-I 18 7 8 4.55 0
4. R36848 Insulin-like growth factor-I 18 7 8 4.55 0
5. P50378 Antigenic peptide fragment of 18 7 8 4.55 0
6. R36910 Insulin-like growth factor-II 20 7 8 4.55 0
7. P40341 IGF-I (26-46). 21 7 8 4.55 0
8. R13324 Cd peptide used in protective 29 7 8 4.55 0
9. P81209 C-domain of IGF-1 (Fra-B-7). 30 7 8 4.55 0
10. P60079 Sequence encoded by peptide C 31 7 8 4.55 0
11. P80431 Sequence of N-terminal portio 35 7 8 4.55 0
12. P90515 Derivative of insulin-like gr 62 7 8 4.55 0
13. P91501 New insulin-like growth facto 67 7 8 4.55 0
14. R36847 Insulin-like growth factor-I 70 7 8 4.55 0
15. R36846 Insulin-like growth factor-I. 70 7 8 4.55 0
16. R33854 IGF-I. 70 7 8 4.55 0
17. P40034 Sequence of human insulin-lik 70 7 8 4.55 0
18. R10587 Modified mammalian somatomedi 70 7 8 4.55 0
19. R10586 Modified mammalian somatomedi 70 7 8 4.55 0
20. P71539 Sequence of human insulin-lik 70 7 8 4.55 0
21. P70414 Sequence of oxidative human i 70 7 8 4.55 0
22. R06306 Human insulin-like growth fac 70 7 8 4.55 0
23. R06307 Human insulin-like growth fac 70 7 8 4.55 0
24. P94660 Analogue IGF252 of human insu 70 7 8 4.55 0
25. P94661 Analogue IGF130 of human insu 70 7 8 4.55 0
26. P93366 Analogue IGF122 of human insu 70 7 8 4.55 0
27. P91502 New insulin-like growth facto 71 7 8 4.55 0
28. R21709 Insulin-like Growth Factor-1. 71 7 8 4.55 0
29. P50872 Synthetic human insulin-like 71 7 8 4.55 0
30. P50098 59-Val insulin-like growth fa 71 7 8 4.55 0
31. P81221 Methionine-insulin-like growt 71 7 8 4.55 0
32. R05281 Synthetic human insulin growt 71 7 8 4.55 0
33. R05281 Amino acid sequence of Insuli 71 7 8 4.55 0
34. P94729 Analogue IGF132 of human insu 72 7 8 4.55 0
35. R11422 Lys-insulin-like Growth Facto 74 7 8 4.55 0
36. R13759 Beta-gal/IGF-1 fusion protein 76 7 8 4.55 0
37. R13758 Beta-gal IGF-1 fusion protein 78 7 8 4.55 0
38. P81213 Insulin-like growth factor-I 89 7 8 4.55 0
39. P40026 Fusion protein of insulin-lik 90 7 8 4.55 0
40. P40024 Short fusion protein contg. i 95 7 8 4.55 0
41. R37549 Sequence of insulin growth fa 95 7 8 4.55 0
42. P82123 Fusion protein of insulin-lik 101 7 8 4.55 0
43. P60077 Sequence encoded by "peptide 103 7 8 4.55 0
44. R13322 Cla protective peptide. 103 7 8 4.55 0
45. R07441 Somatostatin fusion protein. 111 7 8 4.55 0
1. US-08-080-354B-8 (1-13)
R36857 Insulin-like growth factor-I functional derivative
X 10 X
KRPITYGSGRRRK
IIIIIII I
KPTGYGSSSR
X 10
CC The sequence is that of a functional derivative of human insulin-like growth factor (IGF)-I which promotes the survival of retinal neuronal cells. It can be used for the treatment of retinal neuronal tissues which are suffering from the effects of injury, ageing and/or disease such as photodegeneration, trauma, axotomy, neurotoxic-excitatory degeneration, ischemic neuronal degeneration, inherited retinal dystrophy, diabetic retinopathy, Alzheimer's disease, infantile CC malignant osteopetrosis, ceroid lipofuscosi or cholestasis. CC Results of the initial comparison of US-08-080-354B-8 (1-13) with: Data bank : PIR 38, all entries
PARAMETERS
Unitary 1 K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05
Cutoff score 0
Randomization group 0
Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10
SEARCH STATISTICS
Scores: Mean 2 Median 3 Standard Deviation 1.08
Times: CPU 00:01:15.05 Total Elapsed 00:04:07.00
Number of residues: 18022824
Number of sequences searched: 61248
Number of scores above cutoff: 4776
Sequence Name Description Length Score Init. Opt.
1. S12843 *** 5 standard deviations above mean **** 137 8 5.56 0
core antigen - duck hepatitis
2. NKVLHH core antigen - heron hepatitis 305 8 5.56 0

3. NKVLDS core antigen - duck hepatitis 305 8
4. NKVLMD core antigen - duck hepatitis 305 8
5. NKVLBD core antigen - duck hepatitis 305 8
6. NKVLID core antigen - duck hepatitis 305 8
*** 4 standard deviations above mean ***
7. S07198 Insulin-like growth factor - 70 7
8. A37415 Insulin-like growth factor I 70 7
9. A32857 Insulin-like growth factor I 70 7
10. S00465 Insulin-like growth factor I 70 7
11. IG801 Insulin-like growth factor I 70 7
12. A28504 Insulin-like growth factor I 108 7
13. JQ1941 hypothetical 12.8K protein - 116 7
14. A35766 platelet factor 4, interferon 126 7
15. A27849 Insulin-like growth factor IA 127 7
16. JH0133 Insulin-like growth factor I 127 7
17. A25540 Insulin-like growth factor IA 127 7
18. B40912 Insulin-like growth factor I 127 7
19. B25540 Insulin-like growth factor IB 133 7
20. A40912 Insulin-like growth factor I 133 7
21. A34938 Insulin-like growth factor IA 134 7
22. JN0088 Insulin-like growth factor I 137 7
23. A38552 Insulin-like growth factor Ia 137 7
24. IG8P1 Insulin-like growth factor I 137 7
25. S22878 Insulin-like growth factor-I 138 7
26. B33390 Insulin-like growth factor I 138 7
27. S12672 Insulin-like growth factor pr 153 7
28. S12825 Insulin-like growth factor I 153 7
29. S30519 IGF-la - Human 153 7
30. A41399 Insulin-like growth factor IA 153 7
31. A36079 Insulin-like growth factor I 153 7
32. B27804 Insulin-like growth factor IA 153 7
33. IG8U1 Insulin-like growth factor IA 153 7
34. S22877 Insulin-like growth factor-I 154 7
35. A33390 Insulin-like growth factor I 154 7
36. A26859 Insulin-like growth factor IB 159 7
37. A27804 Insulin-like growth factor I 181 7
38. S30540 IGF-lb - Human 195 7
39. A26181 Insulin-like growth factor IB 195 7
40. IG8U1B Insulin-like growth factor IB 195 7
41. JH0550 histone H1t - human 207 7
42. S08031 nucleocapsid protein - human 389 7
43. S15715 chorismate synthase - pink co 447 7
44. A41197 chorismate synthase - pink co 447 7
45. S18153 Serotonin receptor 5HT-dro2A 834 7

1. US-08-080-354B-8 (1-13)

S12843 core antigen - duck hepatitis virus (fragment)

X 10 X

KRKPTGYGSRRRK

|||||

AQGGRKTTTGTRKPRGLPRRRKVKTTVTGRR
80 90 X 100

7. US-08-080-354B-8 (1-13)

S07198 Insulin-like growth factor - Sheep

X 10 X

KRKPTGYGSRRRK

|||||

QFVCGDRGFYENKPTGYGSSRRRAPQTGIVDEC
20 X 30 X 40

Results of the initial comparison of US-08-080-354B-8 (1-13) with:
Data bank : Swiss-Prot 27, all entries

PARAMETERS

Similarity matrix Unitary K-tuple 2
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 13
Gap size penalty 0.05

Cutoff score 0

Randomization group 0

Initial scores to save 45 Alignments to save 15
Optimized scores to save 0 Display context 10

SEARCH STATISTICS

Scores: Mean 2 Median 3 Standard Deviation 0.96

Times: CPU 00:00:48.03 Total Elapsed 00:02:47.00

Number of residues: 11484420
Number of sequences searched: 33329
Number of scores above cutoff: 4163

Sequence Name Description Length Score Init. Opt.

1. CORA_HPBHE CORE ANTIGEN. 305 8 8 6.27 0
2. CORA_HPBDM CORE ANTIGEN. 305 8 8 6.27 0
3. CORA_HPBDU CORE ANTIGEN. 305 8 8 6.27 0
4. CORA_HPBDC CORE ANTIGEN. 305 8 8 6.27 0
5. CORA_HPBDB CORE ANTIGEN. 305 8 8 6.27 0
6. H2BN_STRPU LATE HISTONE H2B.L3. 122 7 7 5.22 0
7. MIG_MOUSE GAMMA INTERFERON INDUCED MONO 126 7 7 5.22 0
8. IGFI_MOUSE INSULIN-LIKE GROWTH FACTOR IA 127 7 8 5.22 0
9. IGFI_CAVPO INSULIN-LIKE GROWTH FACTOR I 130 7 8 5.22 0
10. IGFI_MOUSE INSULIN-LIKE GROWTH FACTOR IB 133 7 8 5.22 0
11. IGFI_RAT INSULIN-LIKE GROWTH FACTOR IA 153 7 8 5.22 0
12. IGFI_HUMAN INSULIN-LIKE GROWTH FACTOR IA 153 7 8 5.22 0
13. IGFI_XENLA INSULIN-LIKE GROWTH FACTOR I 153 7 8 5.22 0
14. IGFI_PIG INSULIN-LIKE GROWTH FACTOR I 153 7 8 5.22 0
15. IGFI_CHICK INSULIN-LIKE GROWTH FACTOR I 153 7 8 5.22 0
16. IGFI_SHEEP INSULIN-LIKE GROWTH FACTOR I 154 7 8 5.22 0
17. IGFI_BOVIN INSULIN-LIKE GROWTH FACTOR I 154 7 8 5.22 0
18. IGFI_RAT INSULIN-LIKE GROWTH FACTOR IB 181 7 8 5.22 0
19. IGFI_HUMAN INSULIN-LIKE GROWTH FACTOR IB 195 7 8 5.22 0
20. H1T_HUMAN HISTONE H1T. 206 7 7 5.22 0
21. AROC_CORSE CHORISMATE SYNTHASE PRECURSOR 447 7 7 5.22 0
22. SHTA_DROME 5-HYDROXYTRYPTAMINE RECEPTOR 834 7 7 5.22 0
23. EBN6_EBV EBNA-6 NUCLEAR PROTEIN (EBNA- 992 7 7 5.22 0

1. US-08-080-354B-8 (1-13)

CORA_HPBHE CORE ANTIGEN.

OS HERON HEPATITIS B VIRUS.

OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; HEPADNAVIRIDAE.

10 X

X

• . .
KRKPTGYGSRRRK

||| | |||

AQGRNQTKGTRKPRGLEPRRRKVKTTVVYGR
240 250 260 270